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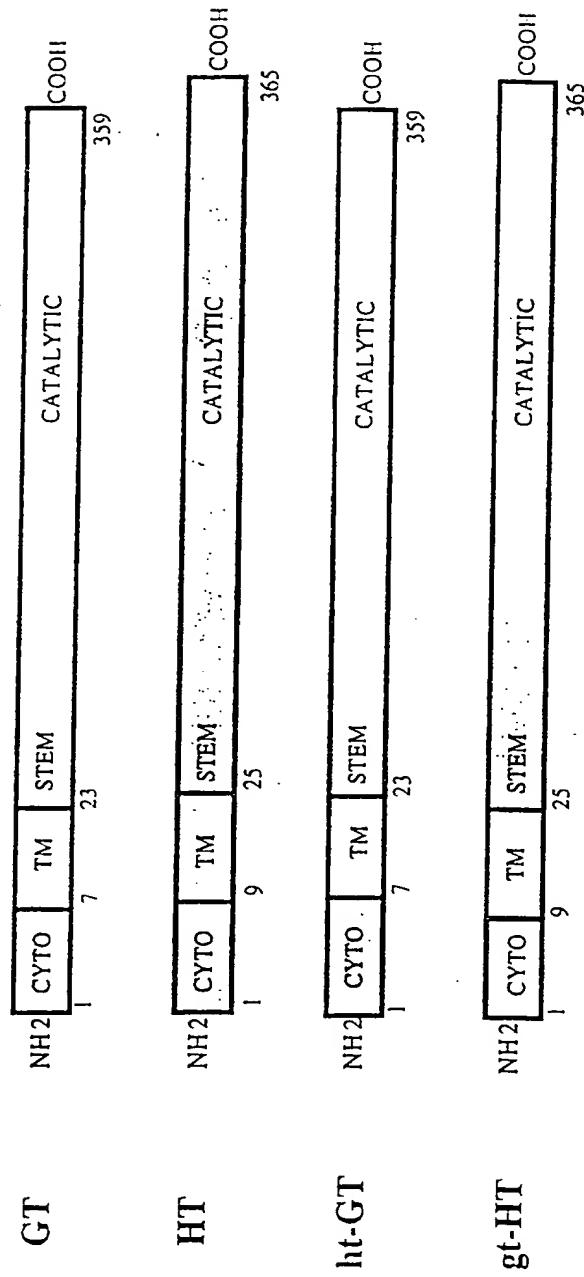


FIGURE 1
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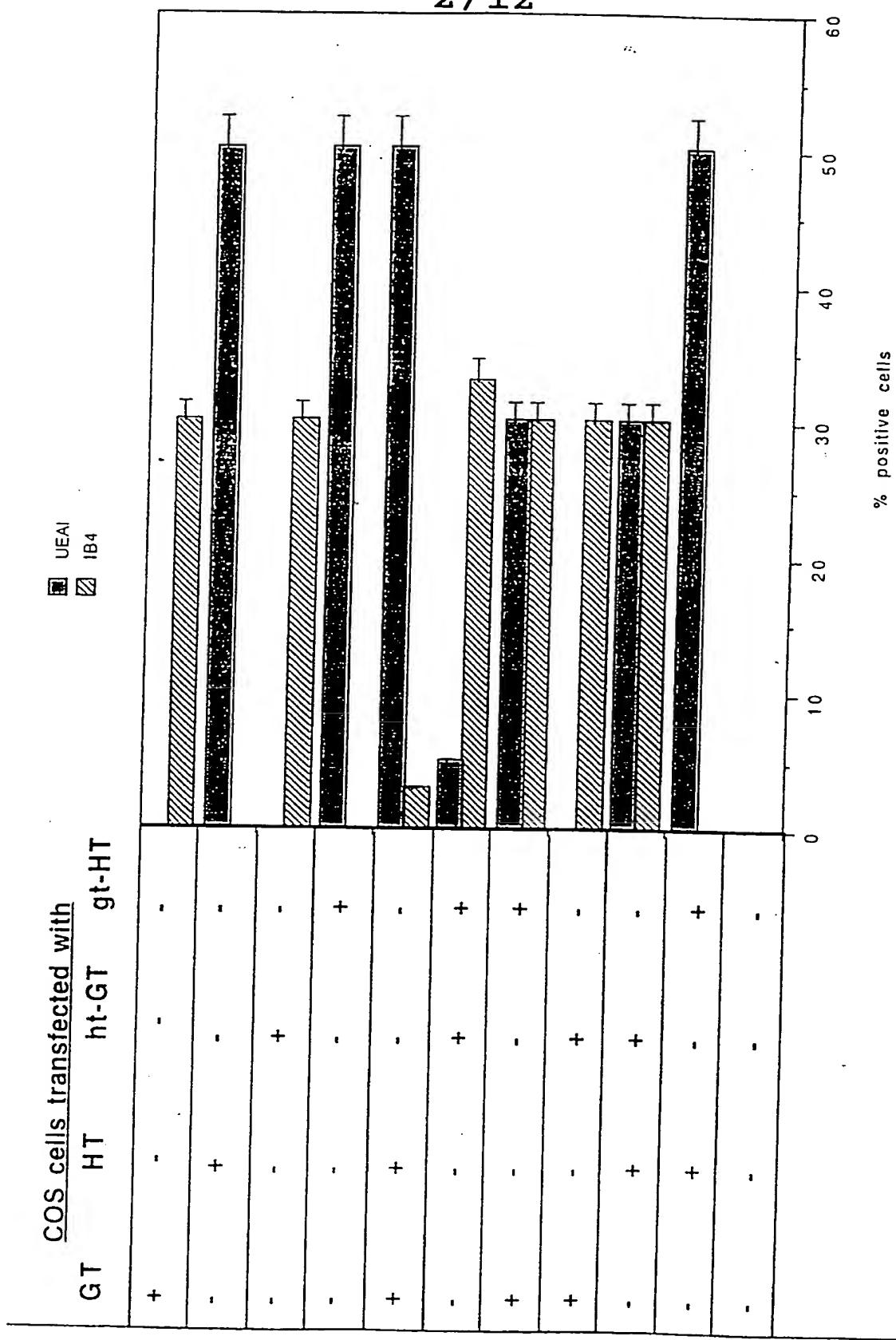


FIGURE 2

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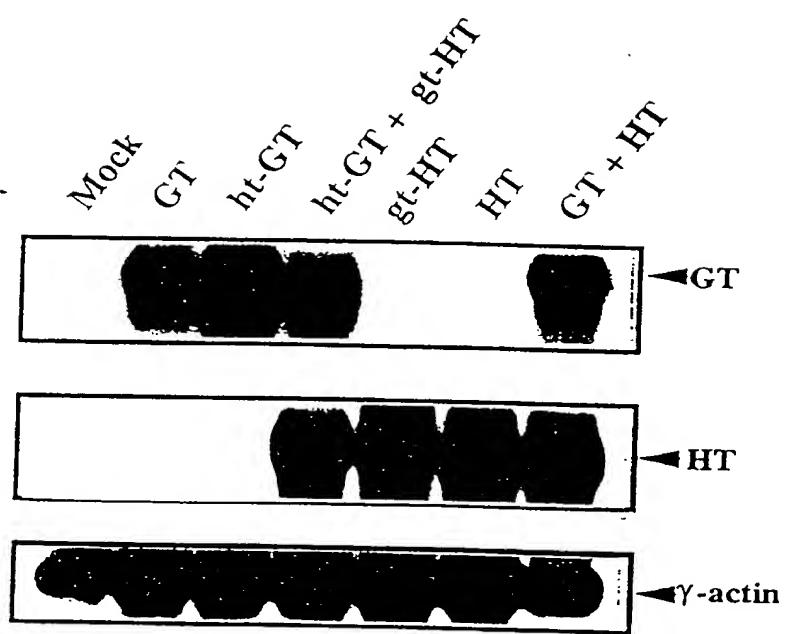


FIGURE 3

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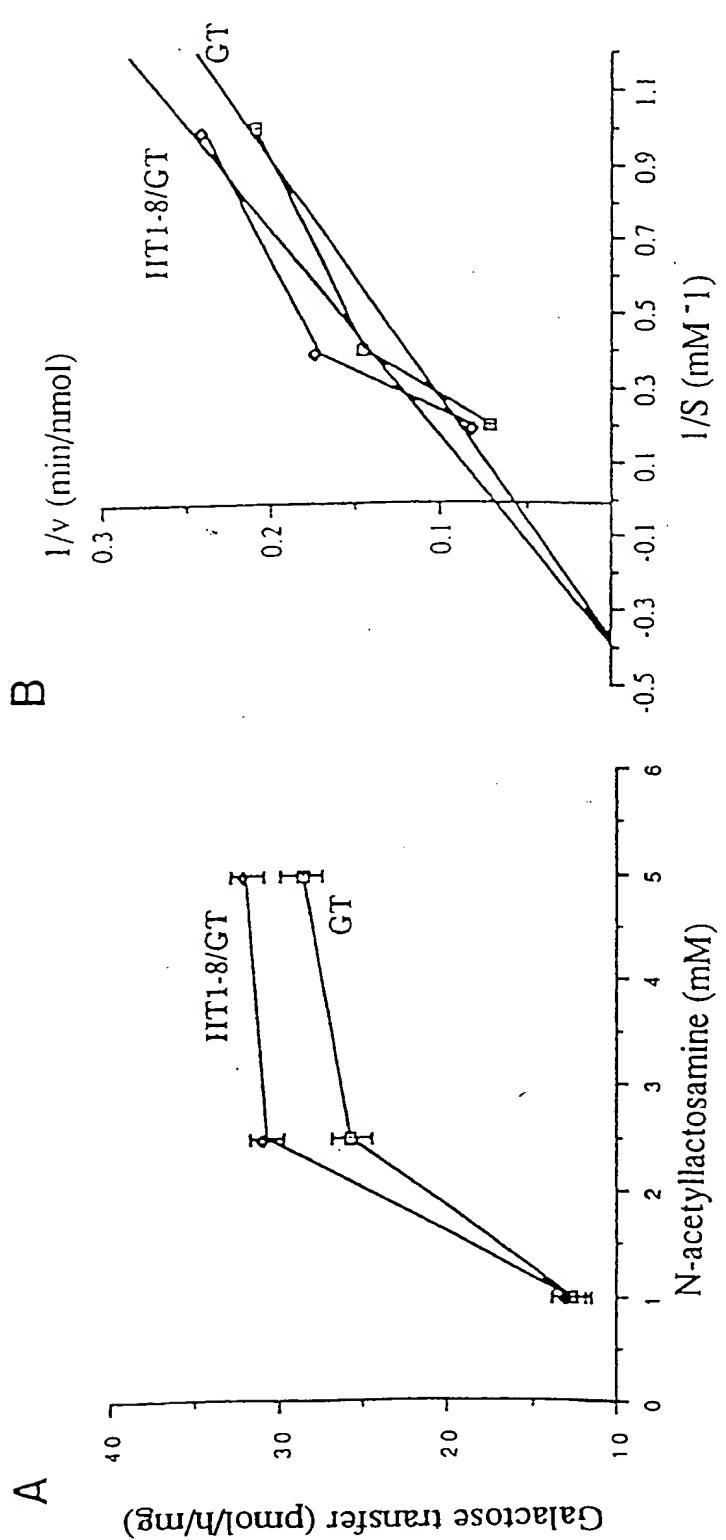


FIGURE 4

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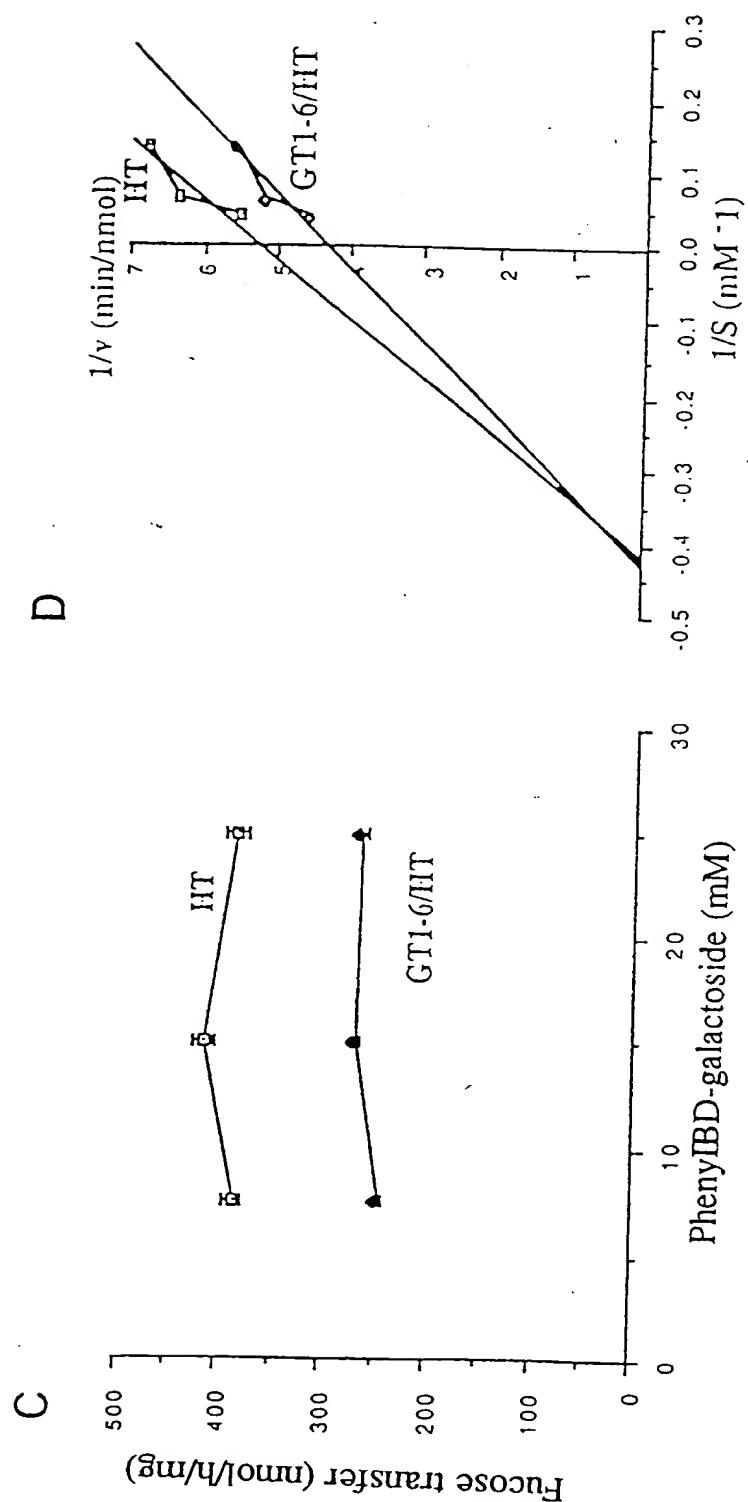


FIGURE 4 Continued

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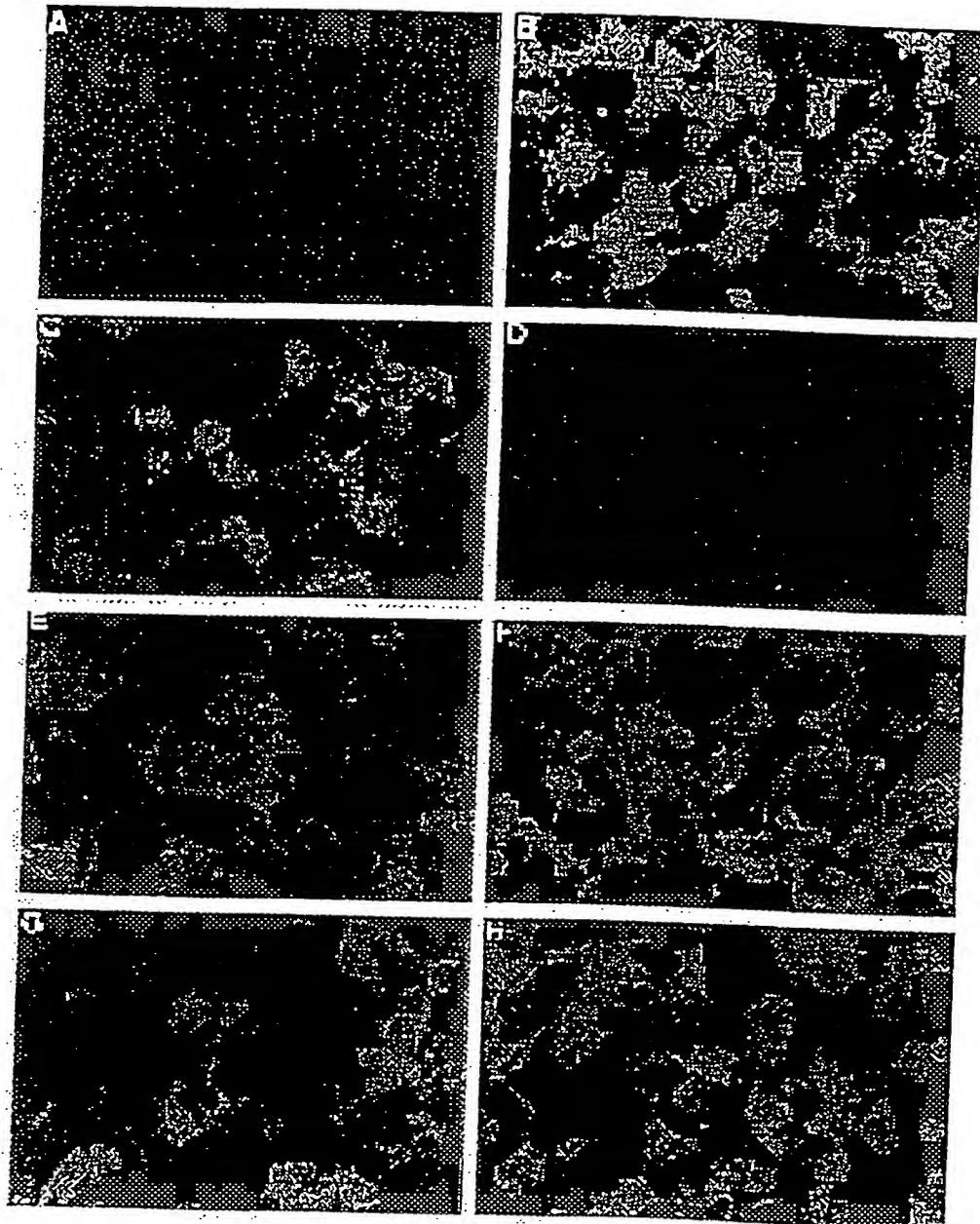


FIGURE 5

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PORCINE SECRETOR SEQUENCE

M	L	S	M	Q	A	S	F	F	P	T	G	P	F	I	L	17				
CT	ACA	GCC	ATG	CTC	AGC	ATG	CAG	GCA	TCC	TTC	TTC	CCC	ACG	GCT	CCC	ATC	CTC	59		
F	V	F	T	A	S	T	I	F	H	L	Q	Q	R	H	V	K	I	Q	37	
TTT	GTC	TTC	ACG	GCT	TCC	ACC	ATA	TTT	CAC	CTT	CAG	CAG	AGG	ATG	GTG	AAG	ATT	CAA	CCC	119
T	W	E	L	Q	M	V	T	Q	V	T	T	E	S	P	S	S	P	Q	L	57
ACG	TGG	GAG	TTA	CAG	ATG	GTG	ACG	CAG	GTG	ACC	ACA	GAG	AGC	CCC	TCG	AGC	CCC	CAG	CTG	179

PORCINE SECRETOR SEQUENCE

K	G	M	W	T	I	N	A	I	G	R	L	G	N	Q	M	G	E	Y	A	77
AAG	GGC	ATG	TGG	ACG	ATC	ATT	GCC	ATC	GGC	CGC	CTG	GGG	AAC	CAG	ATG	GGG	GAG	TAC	GCC	239
T	L	Y	A	L	A	R	M	N	G	R	P	A	F	I	P	P	E	M	H	97
ACC	CTG	TAC	GGC	CTG	GCC	AGG	ATG	AAC	GGG	CGG	CGG	GCC	TTC	ATC	CCG	CCC	GAG	ATG	CAC	299
S	T	L	A	P	I	F	R	I	T	L	P	V	L	H	A	S	T	A	R	117
AGC	ACG	CTG	GGC	CCC	ATC	TTC	AGG	ATC	ACC	CTC	CCG	GTC	CTG	CAC	GCC	ACG	GCC	CGC	359	
R	I	P	W	Q	N	Y	H	L	N	D	W	M	E	E	R	Y	R	H	I	137
AGG	ATC	CCC	TGG	CAG	AAC	TAC	CAC	CTG	AAC	GAC	TGG	ATG	GAG	CGG	TAC	CGC	CAC	ATC	419	
P	G	E	Y	V	R	L	T	G	Y	P	C	S	W	T	F	Y	H	H	L	157

FIGURE 6

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CCG	GGG	GAG	TAC	GTG	CGC	CTC	ACG	GGC	TAC	CCC	TGC	TCC	TGG	ACC	TTC	TAC	CAC	CAC	CTG	479
R	T	E	I	L	R	E	F	T	L	H	N	H	V	R	E	E	A	Q	D	177
CGC	ACC	GAG	ATC	CTC	CGG	GAG	TTC	ACC	CTG	CAT	AAC	CAC	GTG	CGC	GAG	GCC	CAG	GAT	539	
F	L	R	G	L	R	V	N	G	S	R	P	S	T	Y	V	G	V	H	V	197
TTC	CTG	CGG	GGT	CTG	CGG	GTG	AAC	GGG	AGC	CGA	CCG	AGT	ACC	TAC	GTG	GGG	GTG	CAC	GTG	599
R	R	G	D	Y	V	H	V	M	P	N	V	W	K	G	V	V	A	D	R	217
CGC	CGG	GAC	TAC	GTG	CAC	GTG	ATG	CCC	AAC	GTG	TGG	AAG	GGC	GTG	GTG	GCC	GAC	CGG	659	
R	Y	L	E	Q	A	L	D	W	F	R	A	R	Y	R	S	P	V	F	V	237
CGG	TAC	CTG	GAG	CAG	GCC	CTG	GAC	TGG	TTC	CGG	GCT	CGC	TAC	CGC	TCC	CCC	GTC	TTT	GTG	719
V	S	S	N	G	M	A	W	C	R	E	N	I	N	A	S	R	G	D	V	257
GTC	TCC	AGC	AAC	GGC	ATG	GCC	TGG	TGT	CGG	GAA	AAC	ATC	AAT	GCC	TCG	CGC	GAC	GAT	GTG	779
V	F	A	G	N	G	I	E	G	S	P	A	K	D	F	A	L	L	T	Q	277
GTG	TTT	GCC	GCC	AAT	GGC	ATC	GAG	GGC	TCC	CCC	GCC	AAA	GAC	TTC	GCG	CTG	CTC	ACG	CAG	839
C	N	H	T	V	M	T	I	G	T	F	G	I	W	A	A	Y	L	A	G	297
TGT	AAC	CAC	ACT	GTC	ATG	ACC	ATT	GGC	ACG	TTC	GGG	ATC	TGG	GCC	GCC	TAC	CTT	GCT	GGT	899
G	E	T	I	Y	L	A	N	Y	T	L	P	D	S	P	F	L	K	L	F	317
GGA	GAG	ACC	ATC	TAC	CTG	GGC	ATT	TAC	ACG	CTC	CCG	GAC	TCT	CCT	CCC	TTC	AAA	CTC	TTT	959

FIGURE 6 (cont.)

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K P E A A F L P E W I G I E A D L S P L 337
AAG CCC GAG GCA GCC TTC CTG CCC GAG TGG ATT GGG ATC GAG GCA GAC CTG TCC CCA CTC CTC 1019

L K H * 340
CTT AAG CAC TGA TGT CGG CTG TCC 1043

FIGURE 6 (cont.)

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PIG H TRANSFERASE

M W V P S R R H L C L T F L - L V C Y L A	20
ATGTGGGTCCCCAGCCGGGCGACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTAGCA	60
A T F F L N V V Q D L F Y S G L D L L A	40
GCAATTTCCTCCTGAACGTCTATCAAGACCTCTTTACAGTGGCTTAGACCTGCTGGCC	120
L C P D H N V V S S P V A I F C L A G C	60
CTGTGTCAGACCAATAACCTGGTATCATCTCCGTCGCCATATTCTGCCCTGGCGGGCAGC	180
P V H P N A S D S C P K H P A S F S G T	80
CCGGTACACCCCCAACGCCCTCGATTCTGTCCCAACCATCCTGCCCTCTTCCGGGACCC	240
W T I Y P D G R F G N Q M G Q Y A T L D	100
TGGACTATTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG	300
A L A Q L N G R Q A F I Q P A M H A V L	120
GCCCTGGCGCAGCTCACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCCACGCCGTCTG	360
A P V F P I T L P V L A P E V D R H A P	140
CCCCCGTCTCCGCATCACGCTGCCCTGTCTGGCGCCGAGGGTAGACAGGCACGCTCCT	420
W R E L E L H D W M S E D Y A H L K E P	160
TGGCGGGAGCTGGAGCTTACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC	480
W L K L T G F P C S W T F F H H L R E Q	180
TGGCTGAAGCTCACCGCTTCCCTGCTCTGGACCTTCTCCACCACTCCGGAGCAG	540
I R S E F T L H D H L R Q E A Q G V L S	200
ATCCGCAGCGAGTTCACCCCTGCACGACCACCTCGGCAAGAGGGCCAGGGGTACTGAGT	600
Q F R L P R T G D R P S T F V G V H V R	220
CAGTTCCGTCTACCCCGCACAGGGgACCGCCCCAGCACCTCGTGGGGTCCACGTGCGC	660
R G D Y L R V M P K R W K G V V G D G A	240
CGCGGGGACTATCTGCGTGTGATGCCAACGGCTGGAAAGGGGGTGGTGGGTGACGGCGCT	720
Y L Q Q A M D W F R A R Y E A P V F V V	260
TACCTCCAGCAGGCTATGGACTGGTTCGGGGCCGATACGAAGCCCCGTCTTGTGGTC	780
T S N G M E W C R K N I D T S R G D V I	280
ACCAGCAACGGCATGGAGTGGTGGCGGAAGAACATCGACACCTCCGGGGGACGTGATC	840
F A G D G R E A A P A R D F A L L V Q C	300
TTTGGCTGGCGATGGGGGGAGGGCGCCAGGGACTTTGGCTGGTGCAGTGC	900
N H T I M T I G T F G F W A A Y L A G G.	320
AACCACACCATCATGACCAATTGGCACCTTGGCTCTGGCCGCTACCTGGCTGGTGGA	960
D T I Y L A N F T L P T S S F L K I F K	340
GATACCACTACTGGCTAACCTCACCCCTGCCACTTCCAGCTTCTGAAGATCTTAA	1020
P E A A F L P E W V G I N A D L S P L Q	360
CcCGAGGCTGCCCTCGCCAGTGGTGGCATTAATGCAGACTTGTCTCCACTCCAG	1020
M L A G P *	365
ATGTTGGCTGGCCCTTGA	1093

FIGURE 7

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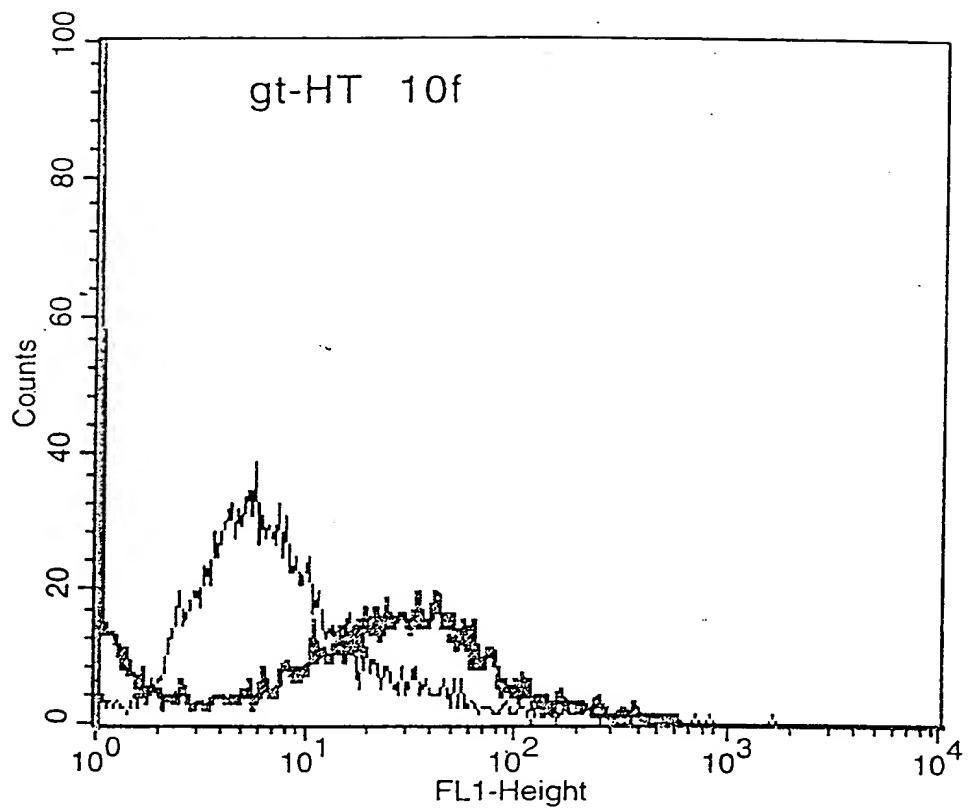


FIGURE 8

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FIGURE 9

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